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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/835,147

DATE: 04/30/2001  
 TIME: 09:22:54

Input Set : A:\2879-US 041201 Seq List.txt  
 Output Set: N:\CRF3\04302001\I835147.raw

P.S

ENTERED

3 <110> APPLICANT: Maliszewski, Charles R.  
 4 Gayle III, Richard B.  
 5 Price, Virginia L.  
 6 Gimpel, Steven D.  
 8 <120> TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
 10 <130> FILE REFERENCE: 2879-US  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/835,147  
 C--> 13 <141> CURRENT FILING DATE: 2001-04-13  
 15 <150> PRIOR APPLICATION NUMBER: US 60/104,585  
 16 <151> PRIOR FILING DATE: 1998-10-16  
 18 <150> PRIOR APPLICATION NUMBER: US 60/107,466  
 19 <151> PRIOR FILING DATE: 1998-11-06  
 21 <150> PRIOR APPLICATION NUMBER: US 60/149,010  
 22 <151> PRIOR FILING DATE: 1999-08-13  
 24 <150> PRIOR APPLICATION NUMBER: PCT/US99/22955  
 25 <151> PRIOR FILING DATE: 1999-10-13  
 27 <160> NUMBER OF SEQ ID NOS: 31  
 29 <170> SOFTWARE: PatentIn Ver. 2.0  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 1599  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Homo sapiens  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: CDS  
 38 <222> LOCATION: (67)..(1596)  
 40 <400> SEQUENCE: 1  
 41 ccacaccaag cagcggctgg gggggggaaa gacgaggaaaa gaggaggaaa acaaaagctg 60  
 43 ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108  
 44 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser  
 45 1 5 10  
 47 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156  
 48 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile  
 49 15 20 25 30  
 51 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204  
 52 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 53 35 40 45  
 55 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252  
 56 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 57 50 55 60  
 59 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300  
 60 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 61 65 70 75  
 63 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348  
 64 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 65 80 85 90  
 67 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396  
 68 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu

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69	95	100	105	110	
71	aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt				444
72	Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val				
73	115	120	125		
75	tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa				492
76	Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu				
77	130	135	140		
79	gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac				540
80	Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn				
81	145	150	155		
83	tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa				588
84	Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu				
85	160	165	170		
87	ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt				636
88	Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser				
89	175	180	185	190	
91	cag aaa aca aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag				684
92	Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln				
93	195	200	205		
95	gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act				732
96	Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr				
97	210	215	220		
99	ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa				780
100	Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln				
101	225	230	235		
103	ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg				828
104	Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu				
105	240	245	250		
107	tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att				876
108	Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile				
109	255	260	265	270	
111	cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga				924
112	Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly				
113	275	280	285		
115	tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc				972
116	Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr				
117	290	295	300		
119	aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt				1020
120	Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly				
121	305	310	315		
123	att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac				1068
124	Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn				
125	320	325	330		
127	acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg				1116
128	Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu				
129	335	340	345	350	
131	cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg				1164
132	Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val				
133	355	360	365		

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135 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	1212
136 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
137 370 375 380	
139 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa	1260
140 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
141 385 390 395	
143 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1308
144 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
145 400 405 410	
147 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1356
148 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr	
149 415 420 425 430	
151 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc	1404
152 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
153 435 440 445	
155 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1452
156 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
157 450 455 460	
159 cca gct gag caa cca ttg tcc aca cct ctc cac tcc acc tat gtc	1500
160 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val	
161 465 470 475	
163 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata	1548
164 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile	
165 480 485 490	
167 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta	1596
168 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val	
169 495 500 505 510	
171 tag	1599
174 <210> SEQ ID NO: 2	
175 <211> LENGTH: 510	
176 <212> TYPE: PRT	
177 <213> ORGANISM: Homo sapiens	
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181 1 5 10 15	
183 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu	
184 20 25 30	
186 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys	
187 35 40 45	
189 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile	
190 50 55 60	
192 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln	
193 65 70 75 80	
195 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln	
196 85 90 95	
198 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala	
199 100 105 110	
201 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu	
202 115 120 125	

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204 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
205 130 135 140  
207 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
208 145 150 155 160  
210 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
211 165 170 175  
213 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
214 180 185 190  
216 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
217 195 200 205  
219 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
220 210 215 220  
222 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
223 225 230 235 240  
225 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
226 245 250 255  
228 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
229 260 265 270  
231 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
232 275 280 285  
234 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
235 290 295 300  
237 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
238 305 310 315 320  
240 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
241 325 330 335  
243 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
244 340 345 350  
246 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
247 355 360 365  
249 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
250 370 375 380  
252 Met Met Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
253 385 390 395 400  
255 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
256 405 410 415  
258 Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
259 420 425 430  
261 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
262 435 440 445  
264 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
265 450 455 460  
267 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
268 465 470 475 480  
270 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
271 485 490 495  
273 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
274 500 505 510  
277 <210> SEQ ID NO: 3

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278 <211> LENGTH: 476  
 279 <212> TYPE: PRT  
 280 <213> ORGANISM: Artificial Sequence  
 282 <220> FEATURE:  
 283 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion  
 284 construct of human CD39  
 286 <400> SEQUENCE: 3  
 287 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys  
 288 1 5 10 15  
 290 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
 291 20 25 30  
 293 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 294 35 40 45  
 296 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 297 50 55 60  
 299 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 300 65 70 75 80  
 302 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 303 85 90 95  
 305 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 306 100 105 110  
 308 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 309 115 120 125  
 311 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 312 130 135 140  
 314 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 315 145 150 155 160  
 317 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 318 165 170 175  
 320 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
 321 180 185 190  
 323 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
 324 195 200 205  
 326 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
 327 210 215 220  
 329 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
 330 225 230 235 240  
 332 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
 333 245 250 255  
 335 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
 336 260 265 270  
 338 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
 339 275 280 285  
 341 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
 342 290 295 300  
 344 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
 345 305 310 315 320  
 347 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
 348 325 330 335

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

**VERIFICATION SUMMARY**  
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L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

4/30/01

file:///C:/CRF3/Outhold/VsrI835147.htm